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BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match: Penalty for a mismatch:

Open gap and extension gap penalties
gap x dropoff expect word size Filter ☐

Sequence 1 Enter accession or GI
or sequence in FASTA format from: to:

DTYIH

Heavy Chain CDR1

Murine 21.6

Sequence 2 Enter accession or GI
or sequence in FASTA format from: to:

SYWMH

residues 50-54 of
Seq ID NO: 15

Align

Clear Input

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov

Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)



[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Help](#)**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]**

Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

Sequence 1 lcl|seq_1 Length 5

Sequence 2 lcl|seq_2 Length 5

No significant similarity was found

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Program Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match: Penalty for a mismatch:

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☐

Sequence 1 Enter accession or GI

Heavy Chain CDR2

or sequence in FASTA format from: to:

RIDPANGYTKYDPKFQG

Murine 21.6

Sequence 2 Enter accession or GI

or sequence in FASTA format from: to:

EIDPSESNTNYNQKFQG

residues 69-85 of
SEQ ID NO: 15

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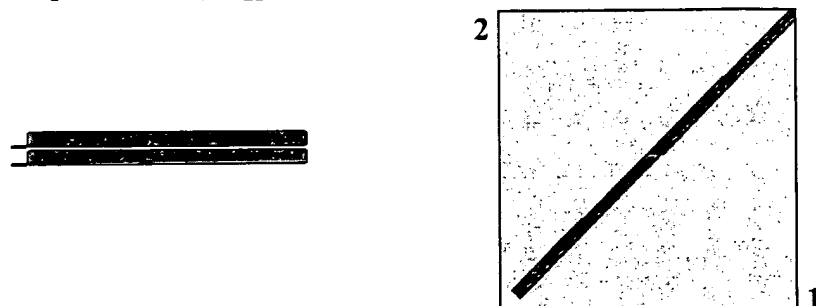
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☐ Align

Sequence 1 lcl|seq_1 Length 17 (1 .. 17)

Sequence 2 lcl|seq_2 Length 17 (1 .. 17)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 22.3 bits (46), Expect = 359
 Identities = 8/16 (50%), Positives = 11/16 (68%)

Query: 2 IDPANGYTKYDPKFQG 17
 IDP+ T Y+ KF+G
 Sbjct: 2 IDPSESNTNYNQKFKG 17

CPU time: 0.03 user secs. 0.02 sys. secs 0.05 total secs.

Gapped:

Lambda K H
 0.270 0.0470 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 6

Number of Sequences: 0

Number of extensions: 1

Number of successful extensions: 1

Number of sequences better than 100000.0: 1

Number of HSP's better than 100000.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 17

length of database: 90,077,593

effective HSP length: 0

effective length of query: 21

effective length of database: 90077593
effective search space: 1891629453
effective search space used: 1891629453

T: 9

A: 40

X1: 17 (7.3 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 29 (15.5 bits)

S2: 26 (14.5 bits)

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Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☐

Sequence 1 Enter accession or GI

or sequence in FASTA format from: to:

EGYFGNYGVYAMDY

Heavy Chain CDR3

21.6 Hc

Sequence 2 Enter accession or GI

or sequence in FASTA format from: to:

GGYDGDYDAIDY

residues 118-129 of
SEQ ID NO: 15

Align

Clear Input

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Matrix: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐

Sequence 1 lcl|seq_1 Length 14

Sequence 2 lcl|seq_2 Length 12

No significant similarity was found